



(1) GENERAL INFORMATION:

(i) APPLICANT: Wainwright, Norman R.
Novitsky, Thomas J.

(ii) TITLE OF INVENTION: Endotoxin Binding and Neutralizing Protein and Uses Thereof

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
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(D) STATE: District of Columbia
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(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 07/883,457
(B) FILING DATE: 15-MAY-1992
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 1413.0010004

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Gly Ile Trp Thr Gln Leu Ile Phe Thr Leu Val Asn Asn Leu Ala
1 5 10 15

Thr Leu Trp Gln Ser Gly Asp Phe Gln Phe Leu Asp His Glu Cys His
20 25 30

Tyr Arg Ile Lys Pro Thr Phe Arg Arg Leu Lys Trp Lys Tyr Lys Gly
35 40 45

Lys Phe Trp Cys Pro Ser Trp Thr Ser Ile Thr Gly Arg Ala Thr Lys
50 55 60

Ser Ser Arg Ser Gly Ala Val Glu His Ser Val Arg Asn Phe Val Gly
65 70 75 80

Gln Ala Gly Ser Ser Gly Leu Ile Thr Gln Arg Gln Ala Glu Gln Phe
85 90 95

Ile Ser Gln Tyr Asn
100

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAG GCT GAA GCT GAC GGT ATC TGG ACC CAA TTG ATT TTC ACT TTG GTT 48
Glu Ala Glu Ala Asp Gly Ile Trp Thr Gln Leu Ile Phe Thr Leu Val
1 5 10 15

AAC ATT TTG GCC ACC TTA TGG CAG TCC GGT GAT TTT CAA TTC TTG GAC 96
Asn Ile Leu Ala Thr Leu Trp Gln Ser Gly Asp Phe Gln Phe Leu Asp
20 25 30

CAC GAA TGT CAC TAC AGA ATC AAG CCA ACT TTC AGA AGA TTG AAG TGG 144
His Glu Cys His Tyr Arg Ile Lys Pro Thr Phe Arg Arg Leu Lys Trp
35 40 45

AAA TAT AAG GGT AAA TTT TGG TGT CCA TCT TGG ACC TCT ATT ACT GGT 192
Lys Tyr Lys Gly Lys Phe Trp Cys Pro Ser Trp Thr Ser Ile Thr Gly
50 55 60

AGA GCT ACC AAG TCT TCT AGA TCC GGT GCT GTC GAA CAC TCT GTT AGA 240
Arg Ala Thr Lys Ser Ser Arg Ser Gly Ala Val Glu His Ser Val Arg
65 70 75 80

AAC TTC GTC GGT CCA GCT AAG TCT TCC GGT TTG ATC ACT GAA AGA CAA 288
Asn Phe Val Gly Pro Ala Lys Ser Ser Gly Leu Ile Thr Glu Arg Gln
85 90 95

GCT GAA CAA TTC ATT TCT CAA TAC AAC TGA TAA GCT TGA ATT C 331
Ala Glu Gln Phe Ile Ser Gln Tyr Asn
100 105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu Ala Glu Ala Asp Gly Ile Trp Thr Gln Leu Ile Phe Thr Leu Val
1 5 10 15

Asn Ile Leu Ala Thr Leu Trp Gln Ser Gly Asp Phe Gln Phe Leu Asp
20 25 30

His Glu Cys His Tyr Arg Ile Lys Pro Thr Phe Arg Arg Leu Lys Trp
35 40 45

Lys Tyr Lys Gly Lys Phe Trp Cys Pro Ser Trp Thr Ser Ile Thr Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Asn Ile Trp Thr Gln Leu Ile Phe Thr Leu Val Asn Asn Leu Ala
 1 5 10 15

Thr Leu Trp Gln Ser Gly Asp Phe Gln Phe Leu Asp His Glu Cys His
 20 25 30

Tyr Arg Ile Lys Pro Thr Phe Arg Arg Leu Lys Trp Lys Tyr Lys Gly
 35 40 45

Lys Phe Trp Cys Pro Ser Trp Thr Ser Ile Thr Gly Arg Ala Thr Lys
 50 55 60

Ser Ser Arg Ser Gly Ala Val Glu His Ser Val Arg Asn Phe Val Gly
 65 70 75 80

Gln Ala Gly Ser Ser Gly Leu Ile Thr Gln Arg Gln Ala Glu Gln Phe
 85 90 95

Ile Ser Gln Tyr Asn
 100

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp	Asn	Ile	Trp	Thr	Gln	Leu	Ile	Phe	Thr	Leu	Val	Asn	Asn	Leu	Ala
1					5				10					15	
Thr	Leu	Trp	Gln	Ser	Gly	Asp	Phe	Gln	Phe	Leu	Asp	His	Glu	Cys	His
						20			25				30		
Tyr	Arg	Ile	Lys	Pro	Thr	Phe	Arg	Arg	Leu	Lys	Trp	Lys	Tyr	Lys	Gly
						35		40				45			
Lys	Phe	Trp	Cys	Pro	Ser	Trp	Thr	Ser	Ile	Thr	Gly	Arg	Ala	Thr	Lys
						50		55			60				
Ser	Ser	Arg	Ser	Gly	Ala	Val	Glu	His	Ser	Val	Arg	Asn	Phe	Val	Gly
65						70				75				80	

Gln Ala Gly Ser Ser Gly Leu Ile Thr Gln Arg Gln Ala Glu Gln Phe
85 90 95

Ile Ser Gln Tyr Asn
100

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Gly Ile Trp Thr Gln Leu Ile Phe Thr Leu Val Asn Asn Leu Ala
1 5 10 15

Thr Leu Trp Gln Ser Gly Asp Phe Gln Phe Leu Asp His Glu Cys His
20 25 30

Tyr Arg Ile Lys Pro Thr Phe Arg Arg Leu Lys Trp Lys Tyr Lys Gly
35 40 45

Lys Phe Trp Cys Pro Ser Trp Thr Ser Ile Thr Gly Arg Ala Thr Lys
50 55 60

Ser Ser Arg Ser Gly Ala Val Glu His Ser Val Arg Asn Phe Val Gly
65 70 75 80

Gln Ala Gly Ser Ser Gly Leu Ile Thr Gln Arg Gln Ala Glu Gln Phe
85 90 95

Ile Ser Gln Tyr Asn
100